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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 01:12:14 ; Search time 159 Seconds
(without alignments)
9532.993 Million cell updates/sec

Title: US-09-847-081B-1

Perfect score: 1728
Sequence: 1 agaaacccagaagaacac.....tcataacccctcaagttag 1728

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1728	100.0	1728	10	US-09-847-081B-1
2	857.8	49.6	1712	10	US-09-847-081B-3
3	806.4	46.7	1239	10	US-09-371-307-75
4	578.4	33.5	1269	9	US-09-938-842A-729
5	52.4	3.0	114	9	US-10-103-450-12
6	52.4	3.0	114	9	US-10-137-765-9
7	52.4	3.0	114	9	US-10-146-337-9
8	41.2	2.4	534	9	US-09-736-457-1310
9	41.2	2.4	534	9	US-09-902-941-1310
10	41.2	2.4	534	9	US-09-849-626-1310
11	41.2	2.4	534	9	US-10-017-754-1310
12	41	2.4	400	9	US-09-938-842A-2919
13	39	2.3	281	10	US-09-369-373-264
14	39	2.3	513509	9	US-09-754-853A-4
15	38.8	2.2	671	9	US-10-184-644-346
16	38.6	2.2	1716	10	US-09-815-242-6522
17	37.6	2.2	684973	10	US-09-263-959-1
18	37.4	2.2	523	9	US-09-796-692-5834
19	37.4	2.2	570	9	US-09-796-692-5383

c 20	37.4	2.2	587	9	US-09-796-692-4936	Sequence 4936, Ap
c 21	37.4	2.2	600	9	US-09-796-692-5328	Sequence 5328, Ap
c 22	37.4	2.2	639	9	US-09-796-692-4925	Sequence 4925, Ap
c 23	37.4	2.2	891	9	US-09-941-947A-33	Sequence 33, Appli
c 24	37.2	2.2	1232	12	US-10-041-472-1	Sequence 1, Appli
c 25	36.8	2.1	11119	10	US-09-764-877-3790	Sequence 3790, Ap
c 26	36.8	2.1	11121	10	US-09-764-877-3791	Sequence 3791, Ap
c 27	36.8	2.1	180557	12	US-10-003-806-9	Sequence 6, Appli
c 28	36.8	2.1	180557	12	US-10-003-806-9	Sequence 9, Appli
c 29	36	2.1	1959	10	US-09-887-586A-27	Sequence 27, Appli
c 30	36	2.1	1959	10	US-09-887-586A-27	Sequence 27, Appli
c 31	35.8	2.1	687	9	US-09-796-692-6578	Sequence 6578, Ap
c 32	35.6	2.1	734	9	US-10-184-644-458	Sequence 458, App
c 33	35.6	2.1	1134	9	US-09-893-519A-127	Sequence 127, App
c 34	35.4	2.0	287	10	US-09-864-761-24815	Sequence 24815, A
c 35	35.4	2.0	575	10	US-09-864-761-8070	Sequence 8070, Ap
c 36	35.4	2.0	1254	9	US-09-989-920-10	Sequence 10, Appli
c 37	35	2.0	1046	10	US-09-925-297-307	Sequence 307, App
c 38	34.6	2.0	524	9	US-10-184-644-204	Sequence 204, App
c 39	34.4	2.0	684973	10	US-09-263-959-1	Sequence 1, Appli
c 40	34.2	2.0	2211	10	US-09-815-242-8548	Sequence 8548, Ap
c 41	34.2	2.0	11474	10	US-09-816-028A-1	Sequence 1, Appli
c 42	34.2	2.0	335913	9	US-09-754-853A-2	Sequence 2, Appli
c 43	34.2	2.0	335913	9	US-09-754-853A-2	Sequence 3, Appli
c 44	34	2.0	516	9	US-09-796-692-8276	Sequence 8276, Ap
c 45	34	2.0	2809	10	US-09-070-927A-434	Sequence 434, App

ALIGNMENTS

RESULT 1
US-09-847-081B-1
: Sequence 1, Application US/09847081B
: Patent No. US2002012846A1
: GENERAL INFORMATION:
: APPLICANT: BAYER AG
: TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
: FILE REFERENCE: Le A 34 326
: CURRENT APPLICATION NUMBER: US/09/847.081B
: CURRENT FILING DATE: 2001-05-02
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1728
: TYPE: DNA
: ORGANISM: Nicotiana tabacum
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (244)..(1566)
US-09-847-081B-1

Query Match	100.0%	Score 1728;	DB 10;	Length 1728;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1728;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AGAAACCCAGAAAGAAACACAGGTTTCTCTCTTGTGATGAGTCATTTGCTCTGCTT	60	
Db	1	AGAAACCCAGAAAGAAACACAGGTTTCTCTCTTGTGATGAGTCATTTGCTCTGCTT	60	
QY	61	GTGTAAGCAAGTCGGTTCATTTCTTATATCCGATTTTATAATCGTTGAAATAGTG	120	
Db	61	GTGTAAGCAAGTCGGTTCATTTCTTATATCCGATTTTATAATCGTTGAAATAGTG	120	
QY	121	GATGACTCTAGTGGATCTACAGTATTTGGTTTTTGTATATAATAGCTGAGTGAGA	180	
Db	121	GATGACTCTAGTGGATCTACAGTATTTGGTTTTTGTATATAATAGCTGAGTGAGA	180	
QY	181	AGGTAACATAAGGAAGAACAAAACTTGGGAATTTTGTAGACACCGAGGTTCTTGT	240	
Db	181	AGGTAACATAAGGAAGAACAAAACTTGGGAATTTTGTAGACACCGAGGTTCTTGT	240	
QY	241	TTCATGAGCATGCTCTGTTGCTTTGTGTGGGTTGTTTCTCCCACTTCCGAGGCTCGAAT	300	

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Db 241 TTATGAGCATCTGTTGCTTTGTTGGGTTGTTTCTCCACTTCCGAGTCTCGAAT 300
QY 301 GGGACAGGATTTGGATTACGTCGAGAGAAACCGCGTCTTTGTATCATCCAGGTTT 360
Db 301 GGGACAGGATTTGGATTACGTCGAGAGAAACCGCGTCTTTGTATCATCCAGGTTT 360
QY 361 CTAGCTCGAGATAGGAATTTGATGTTGATGGAGATCAAGAAAGTGGGAGACAAGG 420
Db 361 CTAGCTCGAGATAGGAATTTGATGTTGATGGAGATCAAGAAAGTGGGAGACAAGG 420
QY 421 TGGATTTTGGCTCTTTAAATTCCTGATCAAGATATTATCATGTTGGTGGATCAAGAAT 480
Db 421 TGGATTTTGGCTCTTTAAATTCCTGATCAAGATATTATCATGTTGGTGGATCAAGAAT 480
QY 481 GAAAGGGAGACATTTCTCTACAGTCCAGTTTGGTGGTGGTGGTGGTGGTGGTGGT 540
Db 481 GAAAGGGAGACATTTCTCTACAGTCCAGTTTGGTGGTGGTGGTGGTGGTGGTGGT 540
QY 541 ACTGTGTCATCAGAGAAAGGCTGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
Db 541 ACTGTGTCATCAGAGAAAGGCTGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
QY 601 AGGCAGCTGAGATCTACCGATGATTAGAAAGTGAAGCCGATATTGTTTCCAGGGAT 660
Db 601 AGGCAGCTGAGATCTACCGATGATTAGAAAGTGAAGCCGATATTGTTTCCAGGGAT 660
QY 661 TTGGGCTTTGAGTGAAGCATATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720
Db 661 TTGGGCTTTGAGTGAAGCATATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720
QY 721 ACATTTTACTTAGGAACCAAGCTAATGATCCCGAGAGAGAAAGGCTATCTGGCAATA 780
Db 721 ACATTTTACTTAGGAACCAAGCTAATGATCCCGAGAGAGAAAGGCTATCTGGCAATA 780
QY 781 TATGTGTGTGCGAGGAAACGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 840
Db 781 TATGTGTGTGCGAGGAAACGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 840
QY 841 CCGCAAGCTTTAGATGTTGGAGACCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
Db 841 CCGCAAGCTTTAGATGTTGGAGACCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
QY 901 GATATGCTTGATGCTGCTTTATCCGATGCTGCTCCAGATTTCTGTTGATATTGAGCA 960
Db 901 GATATGCTTGATGCTGCTTTATCCGATGCTGCTCCAGATTTCTGTTGATATTGAGCA 960
QY 961 TTCAGAGATATGATTGAAGGAATGCGTATGGACTTGTGGAATCCAGATACAAAATTC 1020
Db 961 TTCAGAGATATGATTGAAGGAATGCGTATGGACTTGTGGAATCCAGATACAAAATTC 1020
QY 1021 GATGAGCTATATCTCTATTTGTTTACTATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1080
Db 1021 GATGAGCTATATCTCTATTTGTTTACTATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1080
QY 1081 GTTATGGTATGTCACCTGAATCAAGCAACCAAGCAAGAGAGTATATAATGCTGCTTG 1140
Db 1081 GTTATGGTATGTCACCTGAATCAAGCAACCAAGCAAGAGAGTATATAATGCTGCTTG 1140
QY 1141 GCTTTAGGCTTTGCAAAATCAACTAATATACATCAAGATGTTAGGAGAGATGCCAGA 1200
Db 1141 GCTTTAGGCTTTGCAAAATCAACTAATATACATCAAGATGTTAGGAGAGATGCCAGA 1200
QY 1201 AGAGGAAGAGTATATCTTGCTCAAGATGAAATAGCAGAGGAGGCTCTCCGACGAAGC 1260
Db 1201 AGAGGAAGAGTATATCTTGCTCAAGATGAAATAGCAGAGGAGGCTCTCCGACGAAGC 1260
QY 1261 ATATTGCTGGAAGAGTACTGATGATGAGGAGAACTTTATGAAGAAACAATTCAGAGG 1320
Db 1261 ATATTGCTGGAAGAGTACTGATGATGAGGAGAACTTTATGAAGAAACAATTCAGAGG 1320
QY 1321 GCGAGGAATTTCTTGTGAGTGCAGAGAAAGGTCACAGAACTGACTCTCTAGTAGA 1380
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Db 1321 GCGAGGAATTTCTTGTATGAGTCAGAGAAAGGTCACAGAACTGGACTCTCTAGTAGA 1380
QY 1381 TGGCCTGTGTTTAAACAGCGCTGCTGTTGTTATCGCAAGATATTGGACGAGATTGAAGCAAC 1440
Db 1381 TGGCCTGTGTTTAAACAGCGCTGCTGTTGTTATCGCAAGATATTGGACGAGATTGAAGCAAC 1440
QY 1441 GACTACACAACCTTCCAAAGGAGGCTTATGTTAGCAACCAAGAGCTTCTCAGCTTG 1500
Db 1441 GACTACACAACCTTCCAAAGGAGGCTTATGTTAGCAACCAAGAGCTTCTCAGCTTG 1500
QY 1501 CCATTGTTTATGCAAAATCTCTTGTGCCCCCTAATAGAACTTCCCTCCACTAGCAAG 1560
Db 1501 CCATTGTTTATGCAAAATCTCTTGTGCCCCCTAATAGAACTTCCCTCCACTAGCAAG 1560
QY 1561 ACATGAATGAAGTAGTGTGAGTCAATGAGTATTATAGCACTAAAGAACTCAGGTACTTGA 1620
Db 1561 ACATGAATGAAGTAGTGTGAGTCAATGAGTATTATAGCACTAAAGAACTCAGGTACTTGA 1620
QY 1621 AATGAGATATCTTTGCTAAATGTTGATCATCAAAAGTATGTTAAATTCATATGACA 1680
Db 1621 AATGAGATATCTTTGCTAAATGTTGATCATCAAAAGTATGTTAAATTCATATGACA 1680
QY 1681 ATCTCTTGTAGATATTTTCTCCACTCATCAAAACCTCAAGTGAG 1728
Db 1681 ATCTCTTGTAGATATTTTCTCCACTCATCAAAACCTCAAGTGAG 1728
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RESULT 2

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US-09-847-081B-3
; Sequence 3, Application US/09847081B
; Patent No. US20020128464A1
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
; FILE REFERENCE: Le A 34 326
; CURRENT APPLICATION NUMBER: US/09/847, 081B
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 1712
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (333)..(1565)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 135, 139
; OTHER INFORMATION: Xaa is unknown or other
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 51
; OTHER INFORMATION: n can be any nucleotide
US-09-847-081B-3
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Query Match 49.6%; Score 857.8; DB 10; Length 1712;
Best Local Similarity 76.7%; Pred. No. 4.6e-233;
Matches 1206; Conservative 2; Mismatches 265; Indels 100; Gaps 9;

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QY 132 GTGGATATCTACAAGTATTGGTTTGTATATAAATAGCGTGGAGGAGGTAACATAA 191
Db 218 CAGTAAATTTATTAATTTTATTAATTAAGCAGAGAGGAAGGAACAGAAACAGAA 277
QY 192 AGGAAGACAAAACCTTGGAAATTTGTTAGACCACCGAGGTTCTTGTTCATGAGCAT 251
Db 278 AGTAAGACAAAACCTTGGAAATTTGTTAGAAAGCCAAGGTTTCTCTGTTCAA---AT 334
QY 252 GTCTGTGCTTTGTTGTTGTTGTTTCTCCACTTCCGAGGTCCTCAATGGGACAGATT 311
Db 335 GTCTGTGCTTTGTTGTTGTTGTTTTCAC---CTTGTGAAGTCTCAATGGGACAGATT 391
QY 312 GTTGGATTAGTCCGAGAGGAACCGCGTCTTTGTATCATCAGGTTCTCTAGCTCAGA 371
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Best Local Similarity 79.8%; Pred. No. 4.2e-05;
Matches 75; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

QY 245 TGAGCATGCTGCTGCTTGTGTTGTTCTCCACTCCGAGGTCTCGAATGGGA 304

Db 23 TAAATATGCTGTTGCTTGTATGGTGTGTTCTC---CTGTGACGTCTCAAAATGGGA 79

QY 305 CAGGATGTTGGATTGATCGCGGAGGAACCG 338

Db 80 CAAGTTTCATGGAATCAGTCGGGAGGGAACCG 113

RESULT 8

US-09-736-457-1310/C

; Sequence 1310, Application US/09736457

; Patent No. US20020168637A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; APPLICANT: Wang, Aijun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736.457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1310

; LENGTH: 534

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(534)

; OTHER INFORMATION: n = A,T,C or G

US-09-736-457-1310

Query Match

Best Local Similarity 57.9%; Pred. No. 0.17; Length 534;

Matches 73; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 97 TTTTATATGCTTCAAAATTAAGTGTAGTACTCTAGTGGATATCTACAAAGTATTGGTTT 156

Db 465 TATTTCAAACTTTATCAATAGTGTAAATCTCTAAATGTAATAATCTATGATTTT 406

QY 157 TTGATAAAATAGCTGAGGTGAGAGGTAAACATAAAGGAACAAAACCTTGGGAATTG 216

Db 405 ATACAAAAATCTCTAAAGTCAAAATGTAAGTTAAATCTGTAATAAACATTTTCACCTT 346

QY 217 TTTTAG 222

Db 345 TTCCAG 340

RESULT 9

US-09-902-941-1310/C

; Sequence 1310, Application US/09902941

; Patent No. US20020172952A1

; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Tongtong

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Johnson, Jeffrey C.

; APPLICANT: Retter, Marc W.

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Carter, Darrick

; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.478C17

; CURRENT APPLICATION NUMBER: US/09/902.941

; CURRENT FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 2002

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1310

; LENGTH: 534

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 480, 490

; OTHER INFORMATION: n = A,T,C or G

US-09-902-941-1310

Query Match 2.4%; Score 41.2; DB 9; Length 534;

Best Local Similarity 57.9%; Pred. No. 0.17;

Matches 73; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 97 TTTTATATGCTTCAAAATTAAGTGTAGTACTCTAGTGGATATCTACAAAGTATTGGTTT 156

Db 465 TATTTCAAACTTTATCAATAGTGTAAATCTCTAAATGTAATAATCTATGATTTT 406

QY 157 TTGATAAAATAGCTGAGGTGAGAGGTAAACATAAAGGAACAAAACCTTGGGAATTG 216

Db 405 ATACAAAAATCTCTAAAGTCAAAATGTAAGTTAAATCTGTAATAAACATTTTCACCTT 346

QY 217 TTTTAG 222

Db 345 TTCCAG 340

RESULT 10

US-09-849-626-1310/C

; Sequence 1310, Application US/09849626

; Publication No. US20020197669A1

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya

; APPLICANT: Fanger, Gary

; APPLICANT: Wang, Aijun

; APPLICANT: Wang, Tongtong

; APPLICANT: Switzer, Anne

; APPLICANT: McNeill, Patricia

; APPLICANT: Clapper, Jonathan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C16

; CURRENT APPLICATION NUMBER: US/09/849.626

; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 1926

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1310

; LENGTH: 534

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(534)

; OTHER INFORMATION: n = A,T,C or G

US-09-849-626-1310

Query Match 2.4%; Score 41.2; DB 9; Length 534;

Best Local Similarity 57.9%; Pred. No. 0.17;

Matches 73; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 97 TTTTATATGCTTCAAAATTAAGTGTAGTACTCTAGTGGATATCTACAAAGTATTGGTTT 156

Db 465 TATTTCAAACTTTATCAATAGTGTAAATCTCTAAATGTAATAATCTATGATTTT 406

QY 157 TTGATAAAATAGCTGAGGTGAGAGGTAAACATAAAGGAACAAAACCTTGGGAATTG 216

Db 405 ATACAAAAATCTCTAAAGTCAAAATGTAAGTTAAATCTGTAATAAACATTTTCACCTT 346

Db 465 TATTACAAACTTTATCAATAGTGTAAATCTCTAAATGTAAATAATCTATGGATTT 406
QY 157 TTGATAAAATAGCTGAGGTGAGTAACATAAAGGAAGACAAAACCTTGGGAATTG 216
Db 405 ATACAAAATACCTTAAGTACAAATGTAAGTTAAATGCTGAATAAACAATTTTCACCTT 346
QY 217 TTTTAG 222
Db 345 TTCCAG 340

RESULT 11

US-10-017-754-1310/C
; Sequence 1310, Application US/10017754
; Publication No. US20030034363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihito
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1310
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 480..490
; OTHER INFORMATION: n = A,T,C or G
US-10-017-754-1310

Query Match 2.4%; Score 41.2; DB 9; Length 534;
Best Local Similarity 57.9%; Pred. No. 0.17;
Matches 73; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 97 TTTTATAAAGCTTTGAAATAGTGGATAGACTCTAGTGGATATCTACAAGTATTGGTTT 156
Db 465 TATTACAAACTTTATCAATAGTGTAAATCTCTAAATGTAAATAAATCTATGGATTT 406
QY 157 TTGATAAAATAGCTGAGGTGAGTAACATAAAGGAAGACAAAACCTTGGGAATTG 216
Db 405 ATACAAAATACCTTAAGTACAAATGTAAGTTAAATGCTGAATAAACAATTTTCACCTT 346
QY 217 TTTTAG 222
Db 345 TTCCAG 340

RESULT 12

US-09-938-842A-2919
; Sequence 2919, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2919
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2919

Query Match 2.4%; Score 41; DB 9; Length 400;
Best Local Similarity 50.2%; Pred. No. 0.16;
Matches 101; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 73 GTCGGTTCACTTTCTTATATCCGATTTTATATCGTTGAAATAGTGGATAGACTCTAG 132
Db 103 GTCGTATCGTTGCTTATTCCTTATGCTTGGATAAAGCTTCAATTTTCTCCTCAATTTTG 162
QY 133 TGGATATCTACAAGTATTGGTTTTTGTATATAAATAGCGTGAGGTGAGAGGTACATATAA 192
Db 163 TCGAAAATGTAAACATTTTTTTTGTCTCCACTGTGAGATTGTCACACAGCATTTCTTAAA 222
QY 193 GGAAGACAAAACCTTGGGATTTTGTAGACCACCGAGTTTCTTTTCATGAGCATG 252
Db 223 GAAATGAGACGAATTTTGAACACGATTTATAAATAATAGTATTTTGTCTTCTTGAGCTTA 282
QY 253 TCTGTTGCTTTGTTGTGGGTT 273
Db 283 TCTCCTCTTTCTCTTTGGTT 303

RESULT 13

US-09-969-373-264/C
; Sequence 264, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 264
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-264

Query Match 2.3%; Score 39; DB 10; Length 281;
Best Local Similarity 54.5%; Pred. No. 0.47;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1557 AAAGACATGAATGAAGTAGTTGAGTCAATGAGTATTATACACTAAAGAACTCAGGTACT 1616
Db 196 AGAGAGATAAAAGATAATTTATAACATTTATTATTATGAGCTAAACAAATTAAGGATAT 137
QY 1617 TGTAATGAGATATCTTTTGTCTAAATGTGTATCATCAAAAGTAGTATTTTAATCAATAT 1676
Db 136 TTTAAATGAAAATAATCAATACAAAGAAATAATAAATAAGAGTTTTCGTAATAATGGACAA 77
QY 1677 GACAATCTCTTGGTGAAGATATTT 1699

Db 76 TAAATTTCTTAAAAATATT 54

RESULT 14

US-09-754-853A-4/c
; Sequence 4, Application US/09754853A
; Publication No. US20030005491A1

GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.

; APPLICANT: Parnell, Laurence D.

; APPLICANT: Parsons, Jeremy D.

; APPLICANT: Wang, Ming Li

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE REFERENCE: 38-10(15810)B

; CURRENT APPLICATION NUMBER: US/09/754,853A

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 60/174,880

; NUMBER OF SEQ ID NOS: 1119

; SEQ ID NO 4

; LENGTH: 513509

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (11805)..(113968)..(114684)..(115204)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(513509)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: 318013_region_A3

US-09-754-853A-4

Query Match 2.3%; Score 39; DB 9; Length 513509;

Best Local Similarity 54.5%; Pred. No. 50;

Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1557 AAGACATCAATGAGTAGTGGTGGTCAATGAGTATATACATAAAGAACTCAGGTACT 1616

Db 269804 AGAGAGATAAAGATAATTTTATAACATTTATTATGAGTAAACAAATTAAGGATAT 269745

QY 1617 TGTAAATGAGATATCTTTTGCATAATGTCATCAACAAAGTAGATTGTAAATTCATAT 1676

Db 269744 TTATTTGAATAATCATCATCAAAAGATAATTAATAAGAGTTTGTAAATGGACAA 269685

QY 1677 GACAACTCTTGGTAGAATATT 1699

Db 269684 TAAATTTCTTAAAAATATT 269662

RESULT 15

US-10-184-644-346

; Sequence 346, Application US/10184644

; Publication No. US20030044930A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC227

; CURRENT APPLICATION NUMBER: US/10/184,644

; CURRENT FILING DATE: 2002-06-28

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 346

; LENGTH: 671

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-644-346

Query Match 2.2%; Score 38.8; DB 9; Length 671;

Best Local Similarity 7.7%; Pred. No. 0.92;

Matches 32; Conservative 156; Mismatches 225; Indels 2; Gaps 1;

QY 390 TGGGAGATCAAGAAGGTGGAGACAAAGTGGAAATTTGGCTCTTTAATTCCTGATCC 449

Db 151 DNSGLKRKTPALKMSYKRAKASSDLDOASVSPSEENSESEKTSQDFTPEKKA 210

QY 450 AAGATATTTCATCTTGGGTGGATCAAGAAGTCAAGAAAGGGAAGACACTTCTCTGTACATC 509

Db 211 AVRAPRRGPLGGRKKKAPASDSKADSDGAKPEPVAMARSAS--SSSSSSSSSDSV 268

QY 510 CAGTTTGGTGTAGCCAGCTGGAGAAATGACTGTGTCTATCAGAGAAAGAGTGTATGA 569

Db 269 SVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSEVDRISEWKRDEARRRELE 328

QY 570 TGTGTATTAAAGCAGGAGCTTTAGTGAAGAGGAGCAGCTGAGATCTACCGATGATTAGA 629

Db 329 ARRRREQEELRLREQEKEERERRRERADRGAEARGSGGSGDELREDDPEVKKRKG 388

QY 630 AGTGAAGCCGGATATTGTTTCCAGGGAATTGGGCTTGTTCAGTGAAGCATATGATCG 689

Db 389 RGRPPSSSDSEPEALEEREAKKSAKKPOSSSTEPARKPGQKEKRVPRPEEKQQAQPVKE 448

QY 690 TTGTGGCGAAGTATGTGCAGAGTATGCAGAGATATGCAGAGATTTTACTTAGGAACCAAGTAATGAC 749

Db 449 RTRKSEGEFSMDRKVEKKKEPSVEEKLQKHSFKALKVDSPDKVRCNLNLEELCTQV 508

QY 750 CCCAGAGAGAAAGAGCTATCTGGGCAATATATGTGTGTGTCAGGAGAGACGGAT 804

Db 509 TSOILQKNTDVVATLKKIRRYKANKDMKAAAEVYTRLSRVLPKRIEAVQKYNK 563

Search completed: April 5, 2003, 03:12:02

Job time : 632 secs